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Cortinarius callimorphus, a new species from northern California

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Abstract — Described is *Cortinarius callimorphus*, a new species in subgenus *Phlegmacium* from the coastal woods of northern California, with Sitka spruce to its apparent primary host associate. *Cortinarius callimorphus,* which resembles other members of sect. *Multiformes*, stands out because of its citriform spores. Its closest known relative is *C. polymorphus* from Europe.

Key Words — *Cortinariaceae*, fungal taxonomy, nrITS data

Introduction

The ecosystem of the northernmost coastal region of California (Del Norte, Humboldt, and Mendocino counties) is influenced by high annual precipitation averages (CalFire 2011) that are characteristic of the Pacific Northwest temperate rainforest and which support its dominant conifers —*Picea sitchensis* (Bong) Carrière (Sitka spruce) and *Tsuga heterophylla* (Raf.) Sarg. (western hemlock). The extensive wet forests of the region support a rich fungal diversity. The types of approximately two-thirds of the *Cortinarius* species described from California have been collected in this region (Smith 1939; Ammirati & Smith 1977; Moser & Ammirati 1997, 2000). *Cortinarius callimorphus*, described here, is common under Sitka spruce along the northern Californian coast.

Materials & methods

Methods for morphological studies and DNA extraction, PCR conditions and primers, PCR product clean up, and sequencing are outlined in Bojantchev & Davis (2011). Color codes follow Munsell™ soil color charts (Anonymous 2000). Terminology follows Brandrud et al. (1998). Collections are stored in the private herbarium of the first author or at the University of California herbarium in Berkeley (UC) where noted.

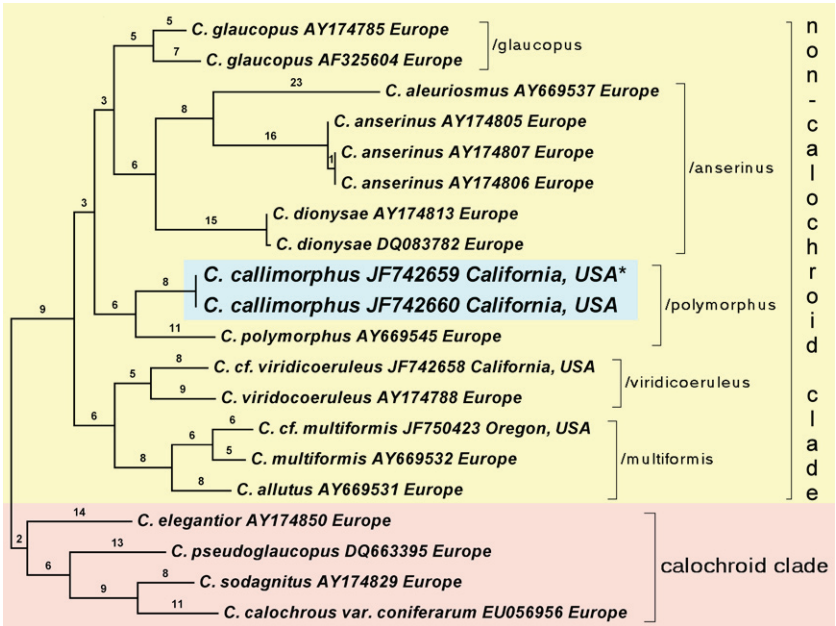

Fig 1. Phylogenetic tree inferred by maximum parsimony analysis of 20 *Cortinarius* subg. *Phlegmacium* nrITS sequences. The tree shows the position of *C. callimorphus* relative to its closest neighboring stirpes and the more distant calochroid clade. Branch lengths represent estimated nucleotide substitutions. The GenBank accession numbers are listed after the taxon names. *Cortinarius calochrous* var. *coniferarum* was selected as outgroup.

Phylogenetic analysis

During our studies we have downloaded and reviewed all *Cortinarius* nrDNA sequences from the public databases GenBank (http://www.ncbi.nlm.nih.gov) and UNITE (http://unite.ut.ee/). Preliminary phylogenetic analysis (not shown) of 984 *Phlegmacium* nrITS sequences from the northern hemisphere, including 278 sequences from our own collections, clarified the closest relatives of *C. callimorphus* and resolved its position outside of the calochroid super-clade as defined by Frøslev et al. (2007) and Garnica et al. (2009).

Twenty *Phlegmacium* taxa were selected for a detailed phylogenetic analysis. Sixteen sequences were sourced from GenBank and four sequences representing western North American taxa came from our collections. The breakdown of the selected sequences is four members of the calochroid super-clade; two sequences of *C. callimorphus* plus one of its closest known relatives; 13 sequences of the most representative taxa of the nearest stirpes to *C. callimorphus* — /anserinus, /viridicoeruleus, /multiformis and /glaucopus from both Europe and Western North America. *Cortinarius calochrous* var. *coniferarum* (M.M. Moser) Nezdojm. was selected as an outgroup.

Sequence alignments were generated with MAFFT v6.821b (Katoh et al. 2002) with the G–INS–i global alignment iterative refinement strategy. Minimal gap opening and

extension penalties were set for better resolution of the more variables sectors within the nrITS. The alignments were visually inspected and corrected where needed.

The evolutionary history was inferred using the Maximum Parsimony method as implemented by MEGA5 (Tamura et al. 2007). The MP trees were generated by the Close-Neighbor-Interchange algorithm with search level 0 in which the initial trees were obtained with the random addition of sequences (10 replicates). The search resulted in nine most parsimonious trees (length = 249) which only differed in the topology of the terminal nodes. One tree was selected (Fig. 1).

Taxonomy

Cortinarius callimorphus Bojantchev & R.M. Davis, **sp. nov.** Figs 2–6

MycoBank MB 561091

Pileo 60–100 mm lato, hemispherico, dein plano-convexo, glutinoso, margine involuto, ochraceoluteo vel flavobrunneo interdum centro, ferrugineo maculato, cum KOH roseobrunneo. Lamellis emarginatis, pallide argillaceis, argillaceobrunneis, in statu senili. Stipite 80–140 mm longo, cylindrico, bulbo submarginato 30–50 mm lato. Velo universale albido. Velo partiale copioso, albido, cum KOH ope nullo. Carne albida. Sapore miti. Sporis 9–10 × 5–6 µm, limoniformibus, verrucosis, basidiis 24–30 × 6–8 µm, tetrasporigeris, fibulis praesentibus.

Type: USA. California: Mendocino County, Caspar, Caspar Cemetery, under *Picea sitchensis*, *22* Nov 2009, Bojantchev DBB25774 (**Holotype** UC 1860824; Genbank nrITS JF742659).

Etymology: from Greek: καλος = beautiful, μορφος = form, shape.

Fig 2. *Cortinarius callimorphus* (collection DBB00080) – a typical form.

straight to involute margin, uniformly ochre yellow (10YR 8/6–8/8), sometimes darker in older basidiomata (10YR 5/6–5/8) with a persistent lighter yellow zone near the margin (2.5Y 8/6) and rusty (5YR 6/6) spots where bruised; surface glutinous when wet, glabrous to dull glossy when dry, innately fibrillose, radially corrugated near the margin at age. Lamellae L = 70–110, crowded, 8–15 mm broad, pale clay (2.5Y 8/1–8/3) to grayish-white when young, never bluish, shading yellow brown to brown (7.5R 6/6–5/6) as the spores mature; edge even; attachment notched; lamellulae abundant. Stipe 80–140 mm long, 10–20 mm wide, cylindrical with a submarginate 30–50 mm wide bulb, white, without bluish tints, spotting brown where bruised. Universal Veil white, leaving volva-like remnants on the bulb. Cortina white, turning rusty brown due to mature spore drop, leaving an annular zone of dense fibrils on the stipe, occasionally forming a hairy appendiculate zone on the pileal margin. Context white, bruising brown. Odor weak, aromatic to none. Taste fungal, not unpleasant. Macrochemical Reactions 5% KOH carmine-red on pileus, uniformly pale yellow brown on context, strongest on mature basidiomata, negative on basal mycelium. UV non-fluorescent. Spore Deposit deep rusty brown.

Basidiospores (8.5–)9.0–10.0(–10.5) × (5.0–)5.2–5.8(–6.0) µm (mean 9.5 × 5.6 µm), Q = 1.54–1.77, Q_{av} = 1.72 (N = 217, 11 basidiomata, seven collections), distinctly citriform, moderately verrucose. Basidia 24–30 × 6–8 µm, 4-spored, cylindro-clavate, clamped. Gill edge fertile or with clusters of elongated septate cells. Cystidia not observed. Pileipellis an ixocutis, duplex; epicutis medium thick, 6–14 layers of hyphae 2–7 µm diam., hyaline, hypodermium well developed, composed of interwoven to parallel cylindrical cells, 20–40 × 12–20 µm with refractive cytoplasmic pigment. Clamp connections common in all parts.

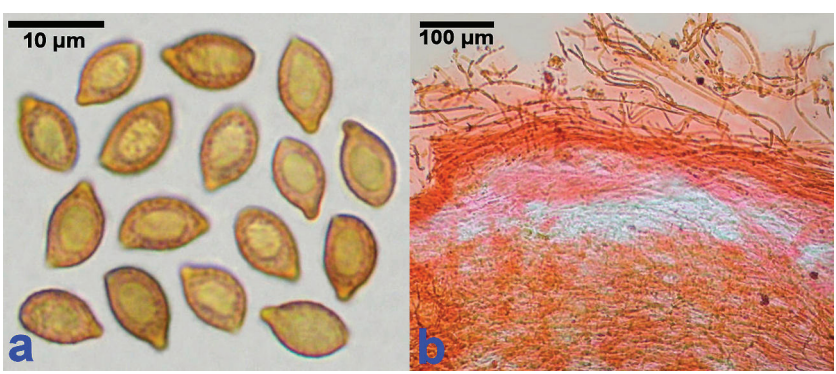

Fig 3. *Cortinarius callimorphus*.
a) Basidiospores (UC 1860824, holotype); b) Cuticle structure (UC 1860824, holotype).

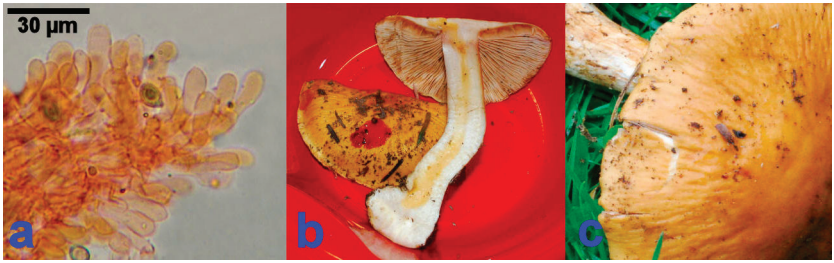

Fig 4. *Cortinarius callimorphus* a) Elongated, septate cells on lamellar edge (UC 1860824, holotype); b) 5% KOH reaction on pileus surface and stipe context (DBB09495); c) Corrugated pileus surface near the margin (DBB09495).

Habitat and distribution — Very common under Sitka spruce in Northern California, particularly in the Mendocino, Humboldt and Del Norte counties. We have never seen it south of Mendocino. Its distribution within the Sitka spruce range is apparently limited to northern California and southern Oregon (where we have collected it once). There are no matching records from Washington and British Columbia despite the intensive collecting and molecular cataloguing that has taken place in these regions. There are no other closely matching North American collections in the public sequence databases.

Fig 5. *Cortinarius callimorphus* collections: a) DBB27800; b) DBB25837.

Fig 6. *Cortinarius callimorphus* collections: a) DBB40200; b) UC 1860824 (holotype)

Additional collections examined: **USA**. **California**: Mendocino County, Caspar, Caspar Cemetery, under *Picea sitchensis*, 26 Nov 2010, Bojantchev DBB40200; 4 Nov 2007, Bojantchev DBB00080; Jackson State Forest, under *Picea sitchensis*, 22 Nov 2008, Bojantchev DBB09495; Jughandle State Reserve, under *Picea sitchensis*, 22 Nov 2009, Bojantchev DBB25837 (UC 1860825, Genbank nrITS JF742660); Del Norte County, Jedediah Smith Redwood State Park, under *Picea sitchensis*, 7 Nov 2009, Bojantchev DBB22704; Humboldt County, Arcata, HBMS Mushroom Fair, under *Picea sitchensis*. 20 Nov 2010, Bojantchev DBB39217; **Oregon**: Curry County, Samuel Boardman State Park, under *Picea sitchensis,* 11 Nov 2009, Bojantchev DBB27800.

Discussion

Traditional morphological analysis based on the overall combination of stature, a yellowish viscid pileus, and argillaceous lamellae suggests that *C. callimorphus* belongs to sect. *Multiformes* Rob. Henry ex Brandr. & Melot. Its carmine-red KOH reaction on the pileus of and submarginate bulb suggest that *C. callimorphus* might be related to the calochroid cortinarii, but its well-developed hypodermium (duplex pileipellis) supports placement in sect. *Multiformes*.

Within that section, *C. callimorphus* stands apart with its distinctly citriform spores, a relatively uncommon feature in the non-calochroid clades. *Cortinarius polymorphus* Rob. Henry is the only other species known with similar macromorphological features (particularly lacking any blue colors) and similarly shaped citriform spores. Detailed descriptions of *C. polymorphus* are available in Henry (1935, 1951, 1985) and Bidaud et al. (2007); the latter includes quality iconography. Molecular analysis confirms a close relationship between the two species (Fig. 1). *Cortinarius polymorphus* has also been assigned to *Multiformes* by Henry (1935, 1951, 1985), Moser (1960), and Bidaud et al. (2007).

Recent phylogenetic studies within *Cortinarius* (Garnica et al. 2003) and our own nrITS analysis show that sect. *Multiformes* is not well supported. Most taxa traditionally assigned to it belong to various other *Phlegmacium* clades. It is not the aim of this work to present a detailed picture of the infrageneric relationships within subg. *Phlegmacium*, but as shown in Fig. 1, *C. callimorphus* and *C. polymorphus* form a clade that is a sibling to the stirpes around *C. viridicoeruleus* Chevassut & Rob. Henry and *C. anserinus* (Velen.) Rob. Henry. A common character of these clades is the distinctly citriform spores.

Cortinarius callimorphus and *C. polymorphus* are very similar but can be separated based on differences in geography (with the former found only in western North America and the latter in Europe), nrITS sequences, and host associations. *Cortinarius polymorphus* is apparently associated with broadleaved trees, mainly members of *Fagaceae*, while *C. callimorphus* is associated with *Picea* and possibly other conifers. The spores of *C. polymorphus* also appear slightly broader with Q_{av} = 1.5 vs. Q_{av} = 1.7 for *C. callimorphus*. Henry (1935)

describes the lamellar edges of *C. polymorphus* as distinctly denticulate, but we have not observed that feature on the *C. callimorphus* basidiomata.

Complete iconography of *C. callimorphus* and a comparative image study is available on http://www.mushroomhobby.com.

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